Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application.

Listing of Claims:

1. (Currently Amended) A computer-based method for identifying conserved peptide motifs useful as drug targets wherein the said method comprises the steps of:

i) providing electronic data representing peptide libraries from the protein sequences of selected organisms,

ii) from the data of step (i), generating computationally overlapping peptide sequences of length 'N', and sorting computationally the peptide sequences of length 'N' according to amino acid sequence,

iii) matching computationally the sorted peptide sequences of length 'N' of the selected organisms to produce matched common peptide sequences,

iv) locating computationally the matched common peptide sequences in the protein sequences of step i) and subsequently labeling the matched common peptide sequences with their origin and location,

v) joining computationally overlapping common peptide sequences to obtain extended conserved peptide sequences,

vi) annotating secondary structure of extended conserved peptide sequences based on a crystal structure database,

vii) ~~comparing pathogenic strain proteomes against proteomes of non-pathogenic strains and selecting at least one conserved peptide sequence not commonly conserved in these two groups,~~ comparing known proteins of a pathogenic organism with those of non-pathogenic organisms using the aforementioned steps (i) to (v), to select at least one conserved peptide

sequence not commonly conserved in both the pathogenic organism and in non-pathogenic organisms, to obtain a consevered peptide sequence,

viii) ~~validating computationally at least one conserved peptide sequence as a potential drug target sequence by searching for a given conserved sequences in the host proteome and rejecting sequences present in the host proteome~~ validating computationaly the conserved peptide sequences obtained in step (vii) as a potential drug target sequences by searching for the conserved peptide sequence in a host proteome.

2. (Previously Amended) The method of claim 1 wherein 'N' is at least 4.

3. (Currently Amended) The method of claim 1 wherein the selected organisms include at least one of: Mycoplasma pneumoniae, Helicobacter pylori, Hemophillus influenzae, Mycobacterium tuberculosis, Mycoplasma genitalium, Bacillus subtillis, and Escherichia coli.

4. (Currently Amended) A method as claimed in claim 1 where conserved peptide motifs as modified comprising sequences include one or more of:

1. AAQSIGEPGTQLT (SEQ ID NO:1)
2. AGDGTTTAT (SEQ ID NO:2)
3. AGRHGNKG (SEQ ID NO:3)
4. AHIDAGKTTT (SEQ ID NO:4)
5. CPIETPEG (SEQ ID NO:5)
6. DEPSIGLH (SEQ ID NO:6)
7. DEPTSALD (SEQ ID NO:7)
8. DEPTTALDVT (SEQ ID NO:8)
9. DHAGIATQ (SEQ ID NO:9)
10. DHPHGGGEG (SEQ ID NO10)
11. DLGGGTFD (SEQ ID NO:11)
35. KMSKSKGN (SEQ ID NO:35)
36. KMSKSLGN (SEQ ID NO:36)
37. KNMITGAAQMDGAILVV (SEQ ID NO:37)
38. KPNSALRK (SEQ ID NO:38)
39. LFGGAGVGKTV (SEQ ID NO:39)
40. LGPSGCGK (SEQ ID NO:40)
41. LHAGGKFD (SEQ ID NO:41)
42. LIDEARTPLIISG (SEQ ID NO:42)
43. LLNRAPTLH (SEQ ID NO:43)
44. LPDKAIDLIDE (SEQ ID NO:44)
45. LPGKLADC (SEQ ID NO:45)

12. DVLDTWFSS (SEQ ID NO:12)
13. ERERGITI (SEQ ID NO:13)
14. ERGITITSAAT (SEQ ID NO:14)
15. ESRRIDNQLRGR (SEQ ID NO:15)
16. FSGGQRQR (SEQ ID NO:16)
17. GEPGVGKTA (SEQ ID NO:17)
18. GFDYLRDN (SEQ ID NO:18)
19. GHNLQEHS (SEQ ID NO:19)
20. GIDLGTTNS (SEQ ID NO:20)
21. GINLLREGLD (SEQ ID NO:21)
22. GIVGLPNVGKS (SEQ ID NO:22)
23. GKSSLLNA (SEQ ID NO:23)
24. GLTGRKIIVDTYG(SEQ ID NO:24)
25. GPPGTGKTLLA (SEQ ID NO:25)
26. GPPGVGKT (SEQ ID NO:26)
27. GSGKTTLL (SEQ ID NO:27)
28. GTRIFGPV (SEQ ID NO:28)
29. IDTPGHVDFT (SEQ ID NO:29)
30. ILAHIDHGKSTL (SEQ ID NO:30)
31. INGFGRIGR (SEQ ID NO:31)
32. IREGGRTVG (SEQ ID NO:32)
33. IVGESGSGKS (SEQ ID NO:33)
34. KFSTYATWWI (SEQ ID NO:34)
46. LSGGQQQR (SEQ ID NO:46)
47. MGHVDHGKT (SEQ ID NO:47)
48. NADFDGDQMAVH (SEQ ID NO:48)
49. NGAGKSTL (SEQ ID NO:49)
50. NLLGKRVD (SEQ ID NO:50)
51. NTDAEGRL (SEQ ID NO:51)
52. PSAVGYQPTLA (SEQ ID NO:52)
53. QRVALARA (SEQ ID NO:53)
54. QRYKGLGEM (SEQ ID NO:54)
55. RDGLKPVHRR (SEQ ID NO:55)
56. SALDVSIQA (SEQ ID NO:56)
57. SGGLHGVG (SEQ ID NO:57)
58. SGSGKSSL (SEQ ID NO:58)
59. SGSGKSTL (SEQ ID NO:59)
60. SVFAGVGERTREGND (SEQ ID NO:60)
61. TGRTHQIRVH (SEQ ID NO:61)
62. TGVSGSGKS (SEQ ID NO:62)
63. TLSGGEAQRI (SEQ ID NO:63)
64. TNKYAEGYP (SEQ ID NO:64)
65. TPRSNPATY (SEQ ID NO:65)
66. VEGDSAGG (SEQ ID NO:66) and
67. VRKRPGMYIG (SEQ ID NO:67).

5. (Previously Amended) A method as claimed in claim 1 comprising increasing the number of [invariant] conserved peptide sequences by increasing the relatedness among the organisms being compared.

6. (Currently Amended) A method as claimed in any one of claims 1-4 wherein the invariant sequences belong to at least one of the following proteins:

I DNA DIRECTED RNA POLYMERASE BETA CHAIN

II EXCINUCLEASE ABC SUBUNIT A

III EXCINUCLEASE ABC SUBUNIT B

IV DNA GYRASE SUBUNIT B

V ATP SYNTHASE BETA CHAIN

VI S-ADENOSYLMETHIONINE SYNTHETASE

VII GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE

VIII ELONGATION FACTOR G (EF-G)

IX ELONGATION FACTOR TU (EF-TU)

X 30S RIBOSOMAL PROTEIN S12

XI 50S RIBOSOMAL PROTEIN L12

XII 50S RIBOSOMAL PROTEIN L14

XIII VALYL tRNA SYNTHETASE (VALRS)

XIV CELL DIVISION PROTEIN FtSH HOMOLOG

XV DnaK PROTEIN (HSP70)

XVI GTP BINDING PROTEIN LepA

XVII TRANSPORTER and

XVIII OLIGOPEPTIDE TRANSPORT ATP BINDING PROTEIN OPPF.

7. (Previously Amended) A method as claimed in claim 1 wherein the said method of comparing the peptide libraries as given in step (iii) of claim 1 is carried out by following the steps:

- selecting organism names from a menu;
- iteratively comparing peptide sequences of a first organism to peptide sequences of a second organism and for matching sequences, writing sequences to a file for the first organism and to a file for the second organism.

8. (Currently Amended) A method as claimed in claim 1 wherein the said method of locating the common peptides in the original protein sequences as given in step (iv) of claim 1 is carried out by following the steps:

- selecting protein sequences;
- iteratively comparing matched peptide sequences to protein sequences;

· ~~where the peptide exists in a protein sequence writing the peptide PID, location and organism in a file associated with that peptide~~ if the peptide is found in a protein sequence, labelling the peptide sequence in a file associated with the protein with: a) a protein identification number (PID), b) a location in the protein sequence, and c) a name of the organism.

9. (Previously Amended) A method as claimed in claim 1 wherein the said method of creating a common peptide of variable length after removing the overlapping as given in step (v) of claim 1 is carried out by following the steps:

· iteratively comparing data on matched peptide locations;

· determining overlapping matched peptides; and

· determining extended peptide sequences based on overlapping matched peptide sequences.

10. (CANCELLED)

11. (CANCELLED)

12. (CANCELLED)